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CHRISTENSON, STEVEN D.
STANDAGE, SCOTT

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ANTIBIOTIC C-1027

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<140> 09/478,188
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<150> 60/115,434
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tcaggaccgc agggtcac 18

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gtggaccaga cgtctacg 18

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 agtccatca agtcsatgrt cgg 23

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ccggtgttsa csgcgtagaa ccaggcg

27

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<210> 105

<211> 18

<212> DNA

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<223> Description of Artificial Sequence: primer

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18

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gcstcccsg acctgggctt cgactc

26

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<211> 26

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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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csggsgssgc sggsttcac gg 22

<210> 109
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<222> (101)..(1096)

<223> sgcA gene

<220>

<221> CDS

<222> (1143)..(2705)

<223> sgcB gene

<400> 112

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Met Arg Met Leu Val
1 5

acg ggc gga gcg ggt ttc atc ggc tcg cag ttc gtg cgg gcc aca ctg 163
Thr Gly Gly Ala Gly Phe Ile Gly Ser Gln Phe Val Arg Ala Thr Leu
10 15 20

cac ggc gag ctg ccg ggt tcc gag gac gcc cgg gtg acg gtc ctg gac 211
His Gly Glu Leu Pro Gly Ser Glu Asp Ala Arg Val Thr Val Leu Asp
25 30 35

aag ctg acg tac tcc ggc aat ccg gcc aac ctc acc tcc gtc gcg gcc 259
Lys Leu Thr Tyr Ser Gly Asn Pro Ala Asn Leu Thr Ser Val Ala Ala
40 45 50

cat ccg cgg tac acc ttc gtc cag ggc gac acc gtc gac ccg cgc gtc 307
His Pro Arg Tyr Thr Phe Val Gln Gly Asp Thr Val Asp Pro Arg Val
55 60 65

gtc gac gag gtg gtc gcc ggc cac gac gtc atc gtc cac ttc gcg gcg 355
Val Asp Glu Val Val Ala Gly His Asp Val Ile Val His Phe Ala Ala
70 75 80 85

gag tcg cac gtg gac cgc tcg atc gac acc gcc acc cgg ttc gtc acg 403
Glu Ser His Val Asp Arg Ser Ile Asp Thr Ala Thr Arg Phe Val Thr
90 95 100

acc aac gtg ctc ggg acc cag acg ctg ctg gaa gcg gct ctc cgg cac 451
Thr Asn Val Leu Gly Thr Gln Thr Leu Leu Glu Ala Ala Leu Arg His
105 110 115

ggg gtc ggc cgg ttc gtg cac gtg tcg acc gac gag gtc tac ggg tcg 499
Gly Val Gly Arg Phe Val His Val Ser Thr Asp Glu Val Tyr Gly Ser
120 125 130

atc gcc tcc ggc tca tgg acc gag gac acc ccg ctc gcc ccc aac gtc 547
Ile Ala Ser Gly Ser Trp Thr Glu Asp Thr Pro Leu Ala Pro Asn Val
135 140 145

ccc tac gcg gcg tcg aag gcg ggt tcg gac ctg atg gcg ctc gcc tgg	595
Pro Tyr Ala Ala Ser Lys Ala Gly Ser Asp Leu Met Ala Leu Ala Trp	
150 155 160 165	
cac cgc acc cgg ggc ctg gac gtc gtc gtc acc cgg tgc acc aac aac	643
His Arg Thr Arg Gly Leu Asp Val Val Val Thr Arg Cys Thr Asn Asn	
170 175 180	
tac ggt ccc tac cag tac ccc gag aag gtg atc ccg ctc ttc gtc acc	691
Tyr Gly Pro Tyr Gln Tyr Pro Glu Lys Val Ile Pro Leu Phe Val Thr	
185 190 195	
aac atc ctc gac ggc ttg cgg gtg ccc ctg tac ggg gac ggc gcc cac	739
Asn Ile Leu Asp Gly Leu Arg Val Pro Leu Tyr Gly Asp Gly Ala His	
200 205 210	
cgc cgg gac tgg ctg cac gtg tcc gac cac tgc cgg gcc atc cag atg	787
Arg Arg Asp Trp Leu His Val Ser Asp His Cys Arg Ala Ile Gln Met	
215 220 225	
gtc atg aac tcc ggc cgg gcc ggg gag gtc tac cac atc ggc ggc ggc	835
Val Met Asn Ser Gly Arg Ala Gly Glu Val Tyr His Ile Gly Gly Gly	
230 235 240 245	
acc gaa ctc tcc aac gag gaa ctc acc ggc ctg ttg ctc acg gcg tgc	883
Thr Glu Leu Ser Asn Glu Glu Leu Thr Gly Leu Leu Leu Thr Ala Cys	
250 255 260	
ggc acc gac tgg tcc tgc gtg gac cgg gtg gcc gac cgg cag ggg cac	931
Gly Thr Asp Trp Ser Cys Val Asp Arg Val Ala Asp Arg Gln Gly His	
265 270 275	
gac cgc cgc tac tcg ctc gac atc acg aag atc cgg cag gaa ctg ggc	979
Asp Arg Arg Tyr Ser Leu Asp Ile Thr Lys Ile Arg Gln Glu Leu Gly	
280 285 290	
tac gag ccc ctg gtc gcc ttc gag gac ggc ctg gcc gcg acg gtg aag	1027
Tyr Glu Pro Leu Val Ala Phe Glu Asp Gly Leu Ala Ala Thr Val Lys	
295 300 305	
tgg tac cac gag aac cgt tcg tgg tgg cag ccg ctg aag gaa gcg gcc	1075
Trp Tyr His Glu Asn Arg Ser Trp Trp Gln Pro Leu Lys Glu Ala Ala	
310 315 320 325	
ggc ctc ctg gac gcc gtc ggc tgacggcagc caccgctagg aacaccccag	1126
Gly Leu Leu Asp Ala Val Gly	
330	
gaaaggagcc acctcc gtg aca gca gtc aag gag ccg acg tcc cgc gca gga	1178
Met Thr Ala Val Lys Glu Pro Thr Ser Arg Ala Gly	
335 340	
cgg cgg gag tgg atc gct ctc gtc gtc ctc tcc ttg ccc acg atg ctg	1226
Arg Arg Glu Trp Ile Ala Leu Val Val Leu Ser Leu Pro Thr Met Leu	
345 350 355 360	

ttg atg ctg gac atc aac gtc ctc atg ctg gcc ttg ccg cag ttg agc	1274
Leu Met Leu Asp Ile Asn Val Leu Met Leu Ala Leu Pro Gln Leu Ser	
365 370 375	
gag gat ctc ggc gcg agc agc acg caa cag ctg tgg atc acc gac atc	1322
Glu Asp Leu Gly Ala Ser Ser Thr Gln Gln Leu Trp Ile Thr Asp Ile	
380 385 390	
tac gga ttc gcg atc gcc ggc ttc ctg gtg acc atg ggc acc ctc ggc	1370
Tyr Gly Phe Ala Ile Ala Gly Phe Leu Val Thr Met Gly Thr Leu Gly	
395 400 405	
gac cgg atc ggc cgc cgc agg ctc ctg ctc ggg ggc gcg gcc gtc ttc	1418
Asp Arg Ile Gly Arg Arg Arg Leu Leu Leu Gly Gly Ala Ala Val Phe	
410 415 420	
gcg gtc gtg tcc gtc gtc gcc gcg ttc tcc gac agc gcg gcg atg ctc	1466
Ala Val Val Ser Val Val Ala Ala Phe Ser Asp Ser Ala Ala Met Leu	
425 430 435 440	
gtc gtc agc cgc gcc gtg ctc ggc gtc gcc ggg gcc acg gtg atg ccc	1514
Val Val Ser Arg Ala Val Leu Gly Val Ala Gly Ala Thr Val Met Pro	
445 450 455	
tcg acg ctc gcg ctc atc agc aac atg ttc gag gac ccc aag gag cgg	1562
Ser Thr Leu Ala Leu Ile Ser Asn Met Phe Glu Asp Pro Lys Glu Arg	
460 465 470	
ggc acc gcc atc gcc atg tgg gcg agc gcc atg atg gcc gga gtc gcc	1610
Gly Thr Ala Ile Ala Met Trp Ala Ser Ala Met Met Ala Gly Val Ala	
475 480 485	
ctc ggg ccc gcc gtc ggc ggc ctg gtc ctc gcc gcg ttc tgg tgg gga	1658
Leu Gly Pro Ala Val Gly Gly Leu Val Leu Ala Ala Phe Trp Trp Gly	
490 495 500	
tcg gtg ttc ctc atc gcc gtt ccg gtg atg ctg ctg gtg gtg gtc acc	1706
Ser Val Phe Leu Ile Ala Val Pro Val Met Leu Leu Val Val Val Thr	
505 510 515 520	
ggc ccc gtg ctg ctc acc gag tcc cgc gac ccg gac gcc gga cgg ctg	1754
Gly Pro Val Leu Leu Thr Glu Ser Arg Asp Pro Asp Ala Gly Arg Leu	
525 530 535	
gac ctg ctg agc gcg ggg ctc tcc ctc gcg acc gtg ctg ccg gtg atc	1802
Asp Leu Leu Ser Ala Gly Leu Ser Leu Ala Thr Val Leu Pro Val Ile	
540 545 550	
tac gga ctg aag gag ctg gcc cgg acc ggg tgg gac ccg ctc gcc gcc	1850
Tyr Gly Leu Lys Glu Leu Ala Arg Thr Gly Trp Asp Pro Leu Ala Ala	
555 560 565	
ggc gcg gtg gtc ctc ggc gtg atc ttc ggc gcg ctg ttc gtc cag cgc	1898
Gly Ala Val Val Leu Gly Val Ile Phe Gly Ala Leu Phe Val Gln Arg	
570 575 580	

cag cgg cgg ttg gcc gac ccc atg ctg gac ctc ggc ctc ttc gcc gac	1946
Gln Arg Arg Leu Ala Asp Pro Met Leu Asp Leu Gly Leu Phe Ala Asp	
585 590 595 600	
cgc acc ctg cgg gcg ggt ctg acg gtc agt ctg gtc aac gcc gtc atc	1994
Arg Thr Leu Arg Ala Gly Leu Thr Val Ser Leu Val Asn Ala Val Ile	
605 610 615	
atg ggc ggg acc gga ctg atg gtc gcc ctg tac ctc cag acg atc gcc	2042
Met Gly Gly Thr Gly Leu Met Val Ala Leu Tyr Leu Gln Thr Ile Ala	
620 625 630	
ggt cac tcc ccg ttg gcc gcc ggg ctg tgg ctg ctg atc ccg gcc tgc	2090
Gly His Ser Pro Leu Ala Ala Gly Leu Trp Leu Leu Ile Pro Ala Cys	
635 640 645	
atg ctc gtc gtg ggc gta cag ctg tgc aac ctg ctg gcc cag cgg atg	2138
Met Leu Val Val Gly Val Gln Leu Ser Asn Leu Leu Ala Gln Arg Met	
650 655 660	
ccc cct tcc cgg gtg ctg ctg ggg gga ctg ctg atc gcg gcc gtc gga	2186
Pro Pro Ser Arg Val Leu Leu Gly Gly Leu Leu Ile Ala Ala Val Gly	
665 670 675 680	
cag ctc ctg atc acc cag gtg gac acc gag gac acc gcc ctc ctc atc	2234
Gln Leu Leu Ile Thr Gln Val Asp Thr Glu Asp Thr Ala Leu Leu Ile	
685 690 695	
gcg gcc acc acc ctg atc tac ttc ggc gcc tca ccg gtg ggg ccg atc	2282
Ala Ala Thr Thr Leu Ile Tyr Phe Gly Ala Ser Pro Val Gly Pro Ile	
700 705 710	
acc acg ggc gcg atc atg gga gcc gcg ccc ccg gag aag gcg ggt gcc	2330
Thr Thr Gly Ala Ile Met Gly Ala Ala Pro Pro Glu Lys Ala Gly Ala	
715 720 725	
gcc tcg tcg ctg tcc gcc acc ggc ggc gag ttc gga gtg gcg ctc ggc	2378
Ala Ser Ser Leu Ser Ala Thr Gly Gly Glu Phe Gly Val Ala Leu Gly	
730 735 740	
atc gcg ggc ctg ggg agt ctg ggc acc gtc gtg tac agc gcc ggg gtc	2426
Ile Ala Gly Leu Gly Ser Leu Gly Thr Val Val Tyr Ser Ala Gly Val	
745 750 755 760	
gag gtg ccg gac gcg gcc ggg ccc gcc gac gcc gac gcc gcg cag gag	2474
Glu Val Pro Asp Ala Ala Gly Pro Ala Asp Ala Asp Ala Ala Gln Glu	
765 770 775	
agc atc gcc ggc gcc ctg cac acg gcc ggt cag ctg gca ccg ggc agc	2522
Ser Ile Ala Gly Ala Leu His Thr Ala Gly Gln Leu Ala Pro Gly Ser	
780 785 790	
gcc gac gcc ctg ctg gac tcc gcg cgc gcg gcc ttc acc agc ggc gtg	2570
Ala Asp Ala Leu Leu Asp Ser Ala Arg Ala Ala Phe Thr Ser Gly Val	
795 800 805	

cag tcc gtc gcc gcc gtc tgc gcc gtg ttc tcc ctg gcg ctc gcc gtc 2618
 Gln Ser Val Ala Ala Val Cys Ala Val Phe Ser Leu Ala Leu Ala Val
 810 815 820

ctc atc ggc acc cgg ctg cgg gac att tcc gcg atg gac cac ggg cac 2666
 Leu Ile Gly Thr Arg Leu Arg Asp Ile Ser Ala Met Asp His Gly His
 825 830 835 840

ggc gag gaa ccg gcc gag aac gac gct caa ccg gcc aca tgagcgact 2715
 Gly Glu Glu Pro Ala Glu Asn Asp Ala Gln Pro Ala Thr
 845 850

tccggagatg caacggccgc cgtcgaggta tgaggatcac cttccgggggt gcacctgcac 2775

ggcaacgggag gcgtagtgga gtactggaac agcacggcgg agaccatgcc ccgccaggaa 2835

ctcgaacagt ggaagtggcg caggctccag gccgccatgg accacgccag aaggctttcg 2895

cccttctggc gggaacgact ccccgagaac atcacctcca tggcggacta cgcggcgcgg 2955

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acctggccct cgctggatcc 3035

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<211> 332

<212> PRT

<213> Streptomyces globisporus

<220>

<223> sgCA

<400> 113

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Val Arg Ala Thr Leu His Gly Glu Leu Pro Gly Ser Glu Asp Ala Arg
 20 25 30

Val Thr Val Leu Asp Lys Leu Thr Tyr Ser Gly Asn Pro Ala Asn Leu
 35 40 45

Thr Ser Val Ala Ala His Pro Arg Tyr Thr Phe Val Gln Gly Asp Thr
 50 55 60

Val Asp Pro Arg Val Val Asp Glu Val Val Ala Gly His Asp Val Ile
 65 70 75 80

Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Asp Thr Ala
 85 90 95

Thr Arg Phe Val Thr Thr Asn Val Leu Gly Thr Gln Thr Leu Leu Glu
 100 105 110

Ala Ala Leu Arg His Gly Val Gly Arg Phe Val His Val Ser Thr Asp
 115 120 125
 Glu Val Tyr Gly Ser Ile Ala Ser Gly Ser Trp Thr Glu Asp Thr Pro
 130 135 140
 Leu Ala Pro Asn Val Pro Tyr Ala Ala Ser Lys Ala Gly Ser Asp Leu
 145 150 155 160
 Met Ala Leu Ala Trp His Arg Thr Arg Gly Leu Asp Val Val Val Thr
 165 170 175
 Arg Cys Thr Asn Asn Tyr Gly Pro Tyr Gln Tyr Pro Glu Lys Val Ile
 180 185 190
 Pro Leu Phe Val Thr Asn Ile Leu Asp Gly Leu Arg Val Pro Leu Tyr
 195 200 205
 Gly Asp Gly Ala His Arg Arg Asp Trp Leu His Val Ser Asp His Cys
 210 215 220
 Arg Ala Ile Gln Met Val Met Asn Ser Gly Arg Ala Gly Glu Val Tyr
 225 230 235 240
 His Ile Gly Gly Gly Thr Glu Leu Ser Asn Glu Glu Leu Thr Gly Leu
 245 250 255
 Leu Leu Thr Ala Cys Gly Thr Asp Trp Ser Cys Val Asp Arg Val Ala
 260 265 270
 Asp Arg Gln Gly His Asp Arg Arg Tyr Ser Leu Asp Ile Thr Lys Ile
 275 280 285
 Arg Gln Glu Leu Gly Tyr Glu Pro Leu Val Ala Phe Glu Asp Gly Leu
 290 295 300
 Ala Ala Thr Val Lys Trp Tyr His Glu Asn Arg Ser Trp Trp Gln Pro
 305 310 315 320
 Leu Lys Glu Ala Ala Gly Leu Leu Asp Ala Val Gly
 325 330

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<212> PRT

<213> Streptomyces globisporus

<220>

<223> sgcB

<400> 114

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Ile Asn Val Leu Met Leu Ala Leu Pro Gln Leu Ser Glu Asp Leu Gly	35		40		45	
Ala Ser Ser Thr Gln Gln Leu Trp Ile Thr Asp Ile Tyr Gly Phe Ala	50		55		60	
Ile Ala Gly Phe Leu Val Thr Met Gly Thr Leu Gly Asp Arg Ile Gly	65		70		75	80
Arg Arg Arg Leu Leu Leu Gly Gly Ala Ala Val Phe Ala Val Val Ser		85		90		95
Val Val Ala Ala Phe Ser Asp Ser Ala Ala Met Leu Val Val Ser Arg		100		105		110
Ala Val Leu Gly Val Ala Gly Ala Thr Val Met Pro Ser Thr Leu Ala		115		120		125
Leu Ile Ser Asn Met Phe Glu Asp Pro Lys Glu Arg Gly Thr Ala Ile		130		135		140
Ala Met Trp Ala Ser Ala Met Met Ala Gly Val Ala Leu Gly Pro Ala		145		150		155
Val Gly Gly Leu Val Leu Ala Ala Phe Trp Trp Gly Ser Val Phe Leu		165		170		175
Ile Ala Val Pro Val Met Leu Leu Val Val Val Thr Gly Pro Val Leu		180		185		190
Leu Thr Glu Ser Arg Asp Pro Asp Ala Gly Arg Leu Asp Leu Leu Ser		195		200		205
Ala Gly Leu Ser Leu Ala Thr Val Leu Pro Val Ile Tyr Gly Leu Lys		210		215		220
Glu Leu Ala Arg Thr Gly Trp Asp Pro Leu Ala Ala Gly Ala Val Val		225		230		235
Leu Gly Val Ile Phe Gly Ala Leu Phe Val Gln Arg Gln Arg Arg Leu		245		250		255
Ala Asp Pro Met Leu Asp Leu Gly Leu Phe Ala Asp Arg Thr Leu Arg		260		265		270
Ala Gly Leu Thr Val Ser Leu Val Asn Ala Val Ile Met Gly Gly Thr		275		280		285
Gly Leu Met Val Ala Leu Tyr Leu Gln Thr Ile Ala Gly His Ser Pro		290		295		300
Leu Ala Ala Gly Leu Trp Leu Leu Ile Pro Ala Cys Met Leu Val Val		305		310		315
						320

Gly Val Gln Leu Ser Asn Leu Leu Ala Gln Arg Met Pro Pro Ser Arg
 325 330 335
 Val Leu Leu Gly Gly Leu Leu Ile Ala Ala Val Gly Gln Leu Leu Ile
 340 345 350
 Thr Gln Val Asp Thr Glu Asp Thr Ala Leu Leu Ile Ala Ala Thr Thr
 355 360 365
 Leu Ile Tyr Phe Gly Ala Ser Pro Val Gly Pro Ile Thr Thr Gly Ala
 370 375 380
 Ile Met Gly Ala Ala Pro Pro Glu Lys Ala Gly Ala Ala Ser Ser Leu
 385 390 395 400
 Ser Ala Thr Gly Gly Glu Phe Gly Val Ala Leu Gly Ile Ala Gly Leu
 405 410 415
 Gly Ser Leu Gly Thr Val Val Tyr Ser Ala Gly Val Glu Val Pro Asp
 420 425 430
 Ala Ala Gly Pro Ala Asp Ala Asp Ala Ala Gln Glu Ser Ile Ala Gly
 435 440 445
 Ala Leu His Thr Ala Gly Gln Leu Ala Pro Gly Ser Ala Asp Ala Leu
 450 455 460
 Leu Asp Ser Ala Arg Ala Ala Phe Thr Ser Gly Val Gln Ser Val Ala
 465 470 475 480
 Ala Val Cys Ala Val Phe Ser Leu Ala Leu Ala Val Leu Ile Gly Thr
 485 490 495
 Arg Leu Arg Asp Ile Ser Ala Met Asp His Gly His Gly Glu Glu Pro
 500 505 510
 Ala Glu Asn Asp Ala Gln Pro Ala Thr
 515 520

<210> 115

<211> 329

<212> PRT

<213> Saccharopolyspora erythraea

<400> 115

Met Arg Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Tyr
 1 5 10 15

Val Arg Gln Leu Leu Gly Gly Ala Tyr Pro Ala Phe Ala Gly Ala Asp
 20 25 30

Val Val Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Glu Glu Asn Leu
 35 40 45

Arg Pro Val Ala Asp Asp Pro Arg Phe Arg Phe Val Arg Gly Asp Ile

50	55	60
Cys Glu Trp Asp Val Val Ser Glu Val Met Arg Glu Val Asp Val Val		
65	70	75 80
Val His Phe Ala Ala Glu Thr His Val Asp Arg Ser Ile Leu Gly Ala		
	85	90 95
Ser Asp Phe Val Val Thr Asn Val Val Gly Thr Asn Thr Leu Leu Gln		
	100	105 110
Gly Ala Leu Ala Ala Asn Val Ser Lys Phe Val His Val Ser Thr Asp		
115	120	125
Glu Val Tyr Gly Thr Ile Glu His Gly Ser Trp Pro Glu Asp His Leu		
130	135	140
Leu Glu Pro Asn Ser Pro Tyr Ser Ala Ala Lys Ala Gly Ser Asp Leu		
145	150	155 160
Ile Ala Arg Ala Tyr His Arg Thr His Gly Leu Pro Val Cys Ile Thr		
	165	170 175
Arg Cys Ser Asn Asn Tyr Gly Pro Tyr Gln Phe Pro Glu Lys Val Leu		
	180	185 190
Pro Leu Phe Ile Thr Asn Leu Met Asp Gly Arg Arg Val Pro Leu Tyr		
	195	200 205
Gly Asp Gly Leu Asn Val Arg Asp Trp Leu His Val Thr Asp His Cys		
210	215	220
Arg Gly Ile Gln Leu Val Ala Glu Ser Gly Arg Ala Gly Glu Ile Tyr		
225	230	235 240
Asn Ile Gly Gly Gly Thr Glu Leu Thr Asn Lys Glu Leu Thr Glu Arg		
	245	250 255
Val Leu Glu Leu Met Gly Gln Asp Trp Ser Met Val Gln Pro Val Thr		
	260	265 270
Asp Arg Lys Gly His Asp Arg Arg Tyr Ser Val Asp His Thr Lys Ile		
	275	280 285
Ser Glu Glu Leu Gly Tyr Glu Pro Val Val Pro Phe Glu Arg Gly Leu		
290	295	300
Ala Glu Thr Ile Glu Trp Tyr Arg Asp Asn Arg Ala Trp Trp Glu Pro		
305	310	315 320
Leu Lys Ser Ala Pro Asp Gly Gly Lys		
	325	

<210> 116

<211> 333
 <212> PRT
 <213> Streptomyces fradiae

<400> 116

Met	Arg	Val	Leu	Val	Thr	Gly	Gly	Ala	Gly	Phe	Ile	Gly	Ser	His	Phe
1				5					10					15	
Thr	Gly	Gln	Leu	Leu	Thr	Gly	Ala	Tyr	Pro	Asp	Leu	Gly	Ala	Thr	Arg
			20					25					30		
Thr	Val	Val	Leu	Asp	Lys	Leu	Thr	Tyr	Ala	Gly	Asn	Pro	Ala	Asn	Leu
			35				40					45			
Glu	His	Val	Ala	Gly	His	Pro	Asp	Leu	Glu	Phe	Val	Arg	Gly	Asp	Ile
	50					55						60			
Ala	Asp	His	Gly	Trp	Trp	Arg	Arg	Leu	Met	Glu	Gly	Val	Gly	Leu	Val
65					70					75					80
Val	His	Phe	Ala	Ala	Glu	Ser	His	Val	Asp	Arg	Ser	Ile	Glu	Ser	Ser
				85					90					95	
Glu	Ala	Phe	Val	Arg	Thr	Asn	Val	Glu	Gly	Thr	Arg	Val	Leu	Leu	Gln
			100					105					110		
Ala	Ala	Val	Asp	Ala	Gly	Val	Gly	Arg	Phe	Val	His	Ile	Ser	Thr	Asp
			115				120					125			
Glu	Val	Tyr	Gly	Ser	Ile	Ala	Glu	Gly	Ser	Trp	Pro	Glu	Asp	His	Pro
	130					135					140				
Val	Ala	Pro	Asn	Ser	Pro	Tyr	Ala	Ala	Thr	Lys	Lys	Ala	Ser	Asp	Leu
145					150					155					160
Leu	Ala	Leu	Ala	Tyr	His	Arg	Thr	Tyr	Gly	Leu	Asp	Val	Arg	Val	Thr
				165					170					175	
Arg	Cys	Ser	Asn	Asn	Tyr	Gly	Pro	Arg	Gln	Tyr	Pro	Glu	Lys	Ala	Val
			180					185					190		
Pro	Leu	Phe	Thr	Thr	Asn	Leu	Leu	Asp	Gly	Leu	Pro	Val	Pro	Leu	Tyr
			195				200					205			
Gly	Asp	Gly	Gly	Asn	Thr	Arg	Glu	Trp	Leu	His	Val	Asp	Asp	His	Cys
	210					215					220				
Arg	Gly	Val	Ala	Leu	Val	Gly	Ala	Gly	Gly	Arg	Pro	Gly	Val	Ile	Tyr
225					230					235					240
Asn	Ile	Gly	Gly	Gly	Thr	Glu	Leu	Thr	Asn	Ala	Glu	Leu	Thr	Asp	Arg
				245					250					255	
Ile	Leu	Glu	Leu	Cys	Gly	Ala	Asp	Arg	Ser	Ala	Leu	Arg	Arg	Val	Ala
			260					265					270		

Asp Arg Pro Gly His Asp Arg Arg Tyr Ser Val Asp Thr Thr Lys Ile
 275 280 285

Arg Glu Glu Leu Gly Tyr Ala Pro Arg Thr Gly Ile Thr Glu Gly Leu
 290 295 300

Ala Gly Thr Val Ala Trp Tyr Arg Asp Asn Arg Ala Trp Trp Glu Pro
 305 310 315 320

Leu Lys Arg Ser Pro Gly Gly Arg Glu Leu Glu Arg Ala
 325 330

<210> 117

<211> 331

<212> PRT

<213> Streptomyces argillaceus

<400> 117

Met Thr Thr Thr Ser Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly
 1 5 10 15

Ser His Tyr Val Arg Thr Leu Leu Gly Pro Arg Gly Val Pro Asp Val
 20 25 30

Thr Val Thr Val Leu Asp Lys Leu Thr Tyr Ala Gly Thr Leu Thr Asn
 35 40 45

Leu Ala Glu Val Ser Asp Ser Asp Arg Phe Arg Phe Val Arg Gly Asp
 50 55 60

Ile Cys Asp Ala Pro Leu Val Asp Asp Leu Leu Ala Val His Asp Gln
 65 70 75 80

Val Val His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Leu Gly
 85 90 95

Ala Ala Asp Phe Val Arg Thr Asn Val Thr Gly Thr Gln Thr Leu Leu
 100 105 110

Asp Ala Ala Leu Arg Gln Gly Ile Glu Thr Phe Val His Ile Ser Thr
 115 120 125

Asp Glu Val Tyr Gly Ser Ile Asp Ala Gly Ser Trp Pro Glu Thr Ala
 130 135 140

Pro Val Ser Pro Asn Ser Leu Tyr Ser Ala Ala Lys Ala Ser Ser Asp
 145 150 155 160

Leu Val Ala Leu Ala Tyr His Arg Thr His Gly Leu Asp Val Arg Val
 165 170 175

Thr Arg Cys Ser Asn Asn Tyr Gly Ser His Gln Phe Pro Glu Lys Val
 180 185 190

Ile Pro Leu Phe Val Thr Ser Leu Leu Asp Gly Arg Glu Val Pro Leu

195						200						205					
Tyr	Gly	Asp	Gly	Thr	Asn	Val	Arg	Asp	Trp	Leu	His	Val	Asp	Asp	His		
210						215						220					
Val	Arg	Ala	Ile	Glu	Leu	Val	Arg	Thr	Gly	Gly	Arg	Ala	Gly	Glu	Val		
225				230				235				240					
Tyr	Asn	Ile	Gly	Gly	Gly	Thr	Glu	Leu	Ser	Asn	Lys	Glu	Leu	Thr	Gln		
			245						250			255					
Leu	Leu	Leu	Asp	Ala	Cys	Gly	Ala	Gly	Trp	Asp	Arg	Val	Arg	Tyr	Val		
			260						265			270					
Thr	Asp	Arg	Lys	Gly	His	Asp	Arg	Arg	Tyr	Ser	Val	Asp	Cys	Thr	Lys		
275						280						285					
Ile	Arg	Arg	Glu	Leu	Gly	Tyr	Arg	Pro	Ala	Arg	Glu	Phe	Gly	Asp	Ala		
290				295				300									
Leu	Ala	Glu	Thr	Val	Ala	Trp	Tyr	Arg	His	His	Arg	Ala	Trp	Trp	Glu		
305				310				315				320					
Pro	Leu	Thr	Arg	Ala	Tyr	Gly	Ala	Val	Ala	Ala							
			325						330								

<210> 118

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6-His tag

<400> 118

His His His His His His

1

5